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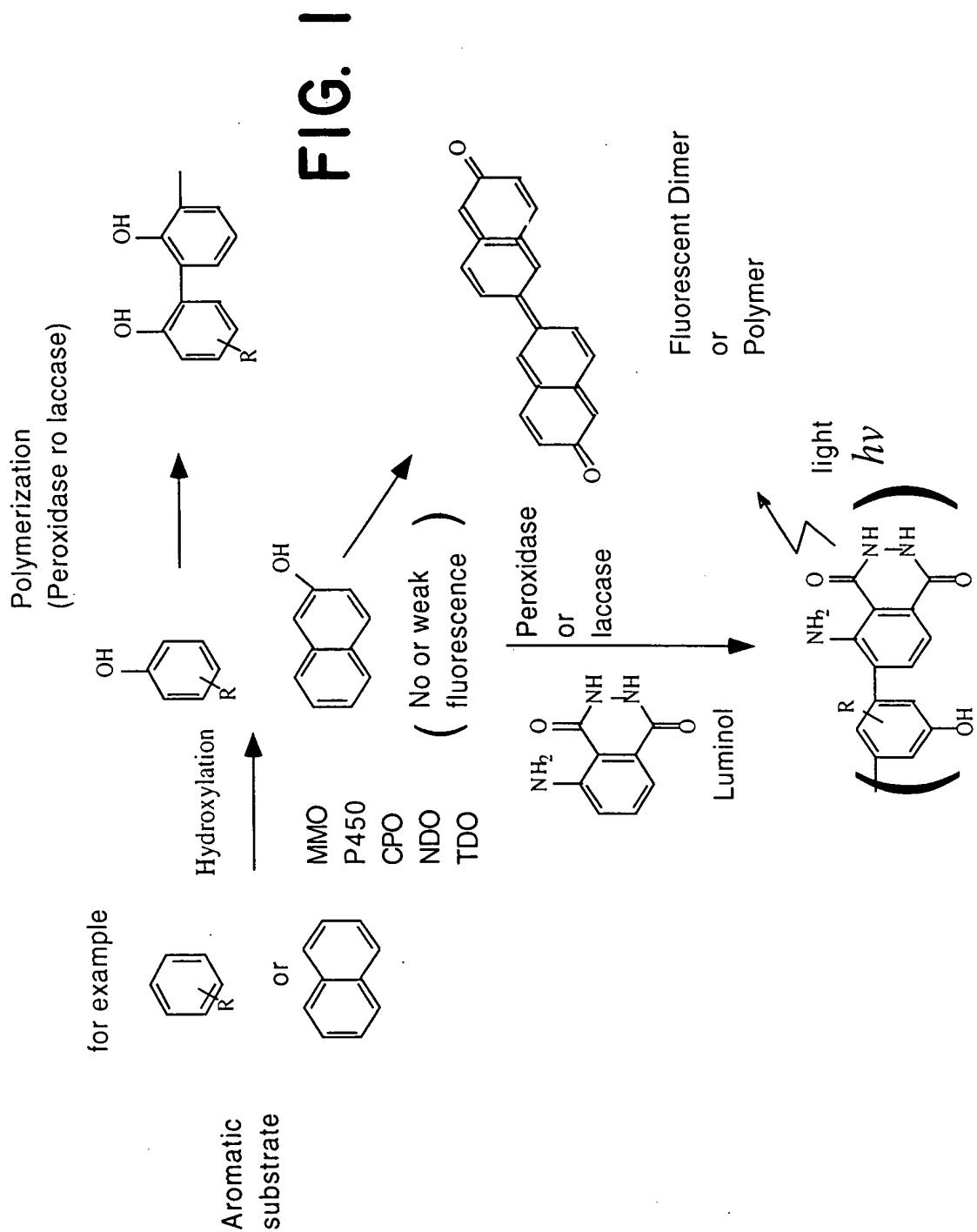
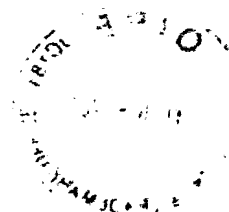


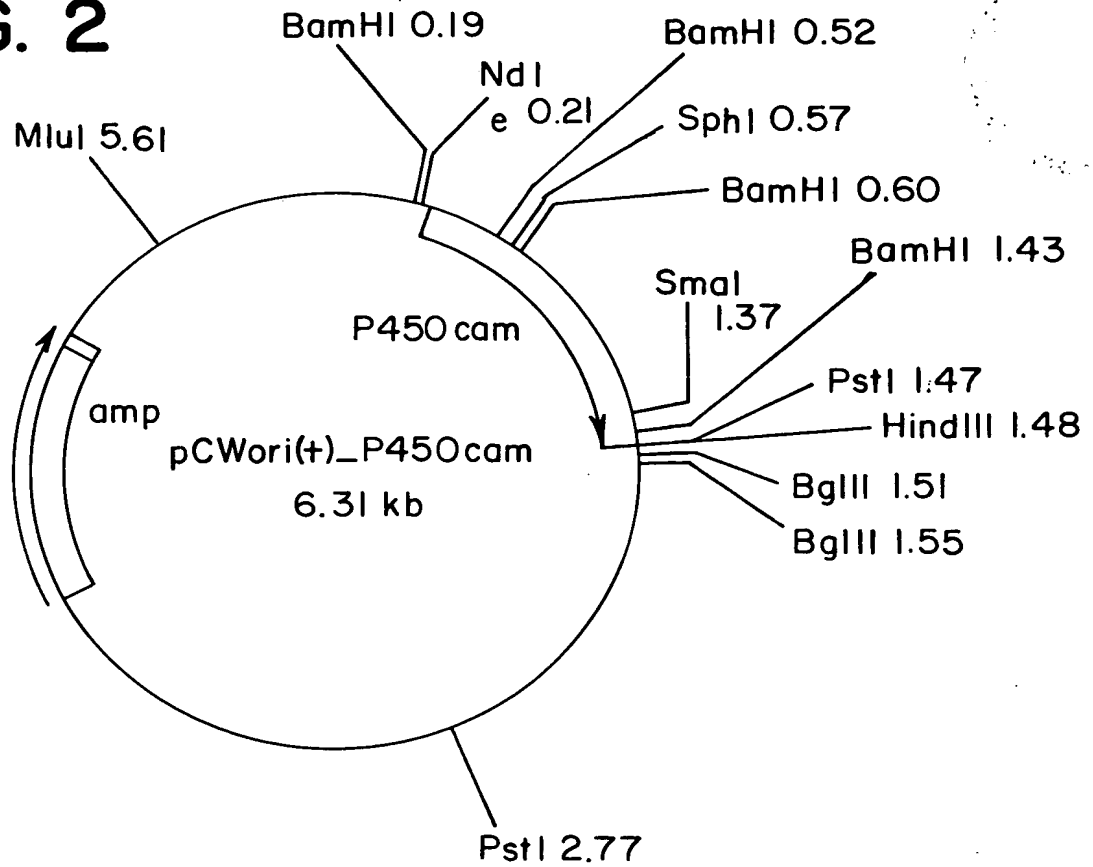
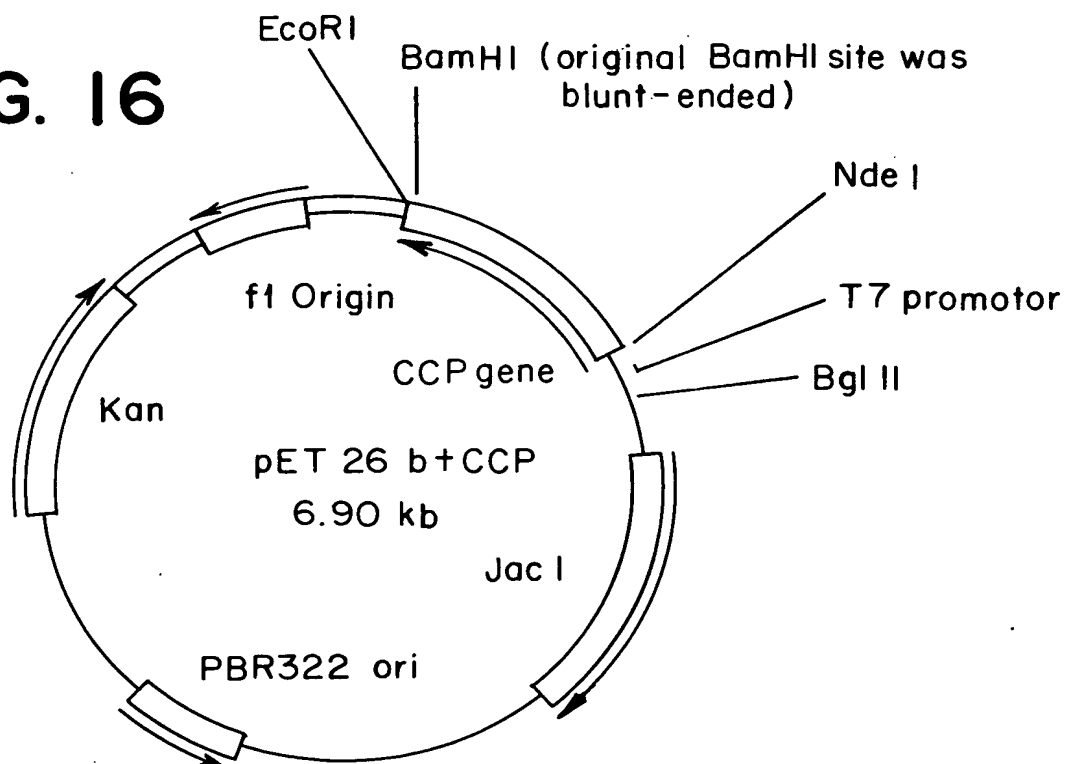
FIG. 2**FIG. 16**

FIG. 3A

1 CTGCAGGATC GTTATCCGCT GCGCATCTG ATCACCCAGC GTTTTTCAT CGACGAGGC
 61 AGCAAGGCAC TTGAACCTGGT CAAGGCAGGA GCACTGATCA AACCGTGAT CGACTCCACT
 121 CTTTAGCCAA CCGCGTTCC AGGAGAACA CAACATGAC GACTGAAACC ATACAAAGCA
 181 AGCCCAATCT TGCCCCCTCTG CCACCCCATG TGCCAGAGCA CCTGGTATTC GACTTOGACA
 241 TGTACAATCC GTGAAATCTG TCTGCGGGG TGCAGGAGGC CTGGCAGTT CTGCAAGAAT
 301 CAAAGTACC GGATCTGGTG TGGACTGGCT GCAAGGGGG ACACGTGATC GGCACCTGGG
 361 GCCAAGTAT CCGTGAGGC TATGAAGATT ACGGCACCT TTCCAGCGAG TGCCCCGTTCA
 421 TCCCTCGTGA AGCGGGGAA GCTACGACT TCATTCCAC CTGATGGAT CCGCCCGAGC
 481 AGGCGCAGTT TGTGCGCTG GCAACCAAG TGGTGGCAT GCGGTGGTG GATTAAGCTGG
 541 AGAACCGGAT CCAGGAGCTG GCTGCTGCG TGATOGAGAG CCTGGCGCG CAGGACAGT
 601 GCAACTTCAC CGAGGACTAC GCGAACCTT TCCGATAAG CATCTTCATG CTGCTGCGAG
 661 GTCTACCGA AGAAGATATC CCGCACTTGA AATACTAAC GATCAGATG ACCGTOGGG
 721 ATGGCAGCAT GAOCCTGCA GAGGCAAGG AGCGCTCTA CGACTATCTG ATACGATCA
 781 TOGAGCAAG CAGGCAGAAG CCGGAAOAG ACGCTATCAG CATCGTTGOC AACGGCCAGG
 841 TCAATGGGG ACGATCACC AGTGACGAAG CCAAGAGGAT GTGTGGCCTG TTAGTGGTOG
 901 GCGGCTGGA TAOGGTGGTC AATTCTCTA GCCTTCAGAT GGAGTCTCTG GCAAAAGCC
 961 CGGAGCATOG CCAGGAGCTG ATGAGGCTC CCGAGGATAT TCCAGCGGCT TGCGAGGAAC
 1021 TACTOOGGG CTCTGCGCTG GTTGOAGTG GCGCATCTT CACCTOOGAT TAAGATTTTC
 1081 ATGGGTGCA ACTGAAGAA GGTGACAGA TCTGTACC GCAGATGCTG TCTGGCCTGG
 1141 ATGAGGCGA AAAGCCTGC CCGATGCAAG TCGACTTCAG TCGCCAAAG GTTTCACACA
 1201 CCACCTTTGG CCACGGCAGC CATCTGTGC TTGGCCAGCA CCTGGCCCGC CGGGAATCA
 1261 TCGTCACCT CAAGGAATGG CTGAOCAGGA TTCTGACTT CTCATTTGCC CCGGTGCCC
 1321 AGATTACGA CAAGAGCGGC ATGTCAGOG GGTGCGAGC ACTCCCTCTG GTCCTGGATC
 1381 CGGCGACTAC CAAAGGGTA TA

FIG. 3B

THR THR GLU THR ILE GLN SER ASN ALA ASN LEU ALA PRO
LEU PRO PRO HIS VAL PRO GLU HIS LEU VAL PHE ASP PHE
ASP MET TYR ASN PRO SER ASN LEU SER ALA GLY VAL GLN
GLU ALA TRP ALA VAL LEU GLN GLU SER ASN VAL PRO ASP
LEU VAL TRP THR ARG CYS ASN GLY GLY HIS TRP ILE ALA
THR ARG GLY GLN LEU ILE ARG GLU ALA TYR GLU ASP TYR
ARG HIS PHE SER SER GLU CYS PRO PHE ILE PRO ARG GLU
ALA GLY GLU ALA TYR ASP PHE ILE PRO THR SER MET ASP
PRO PRO GLU GLN ARG GLN PHE ARG ALA LEU ALA ASN GLN
VAL VAL GLY MET PRO VAL VAL ASP LYS LEU GLU ASN ARG
ILE GLN GLU LEU ALA CYS SER LEU ILE GLU SER LEU ARG
PRO GLN GLY GLN CYS ASN PHE THR GLU ASP TYR ALA GLU
PRO PHE PRO ILE ARG ILE PHE MET LEU LEU ALA GLY LEU
PRO GLU GLU ASP ILE PRO HIS LEU LYS TYR LEU THR ASP
GLN MET THR ARG PRO ASP GLY SER MET THR PHE ALA GLU
ALA LYS GLU ALA LEU TYR ASP TYR LEU ILE PRO ILE ILE
GLU GLN ARG ARG GLN LYS PRO GLY THR ASP ALA ILE SER
ILE VAL ALA ASN GLY GLN VAL ASN GLY ARG PRO ILE THR
SER ASP GLU ALA LYS ARG MET CYS GLY LEU LEU LEU VAL
GLY GLY LEU ASP THR VAL VAL ASN PHE LEU SER PHE SER
MET GLU PHE LEU ALA LYS SER PRO GLU HIS ARG GLN GLU
LEU ILE GLU ARG PRO GLU ARG ILE PRO ALA ALA CYS GLU
GLU LEU LEU ARG ARG PHE SER LEU VAL ALA ASP GLY ARG
ILE LEU THR SER ASP TYR GLU PHE HIS GLY VAL GLN LEU
LYS LYS GLY ASP GLN ILE LEU LEU PRO GLN MET LEU SER
GLY LEU ASP GLU ARG GLU ASN ALA CYS PRO MET HIS VAL
ASP PHE SER ARG GLN LYS VAL SER HIS THR THR PHE GLY
HIS GLY SER HIS LEU CYS LEU GLY GLN HIS LEU ALA ARG
ARG GLU ILE ILE VAL THR LEU LYS GLU TRP LEU THR ARG
ILE PRO ASP PHE SER ILE ALA PRO GLY ALA GLN ILE GLN
HIS LYS SER GLY ILE VAL SER GLY VAL GLN ALA LEU PRO
LEU VAL TRP ASP PRO ALA THR THR LYS ALA VAL

FIG. 4A

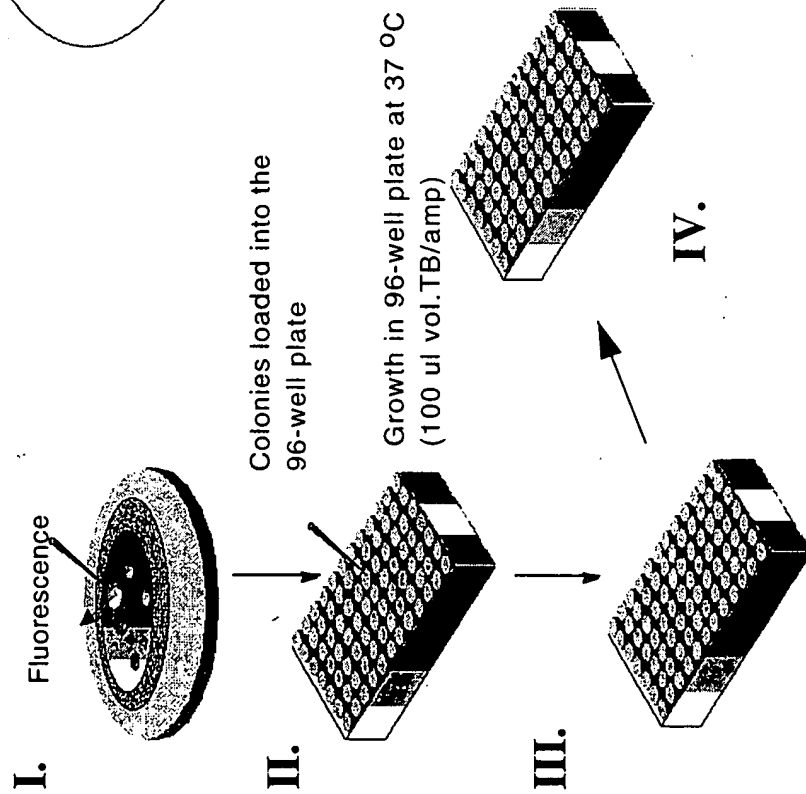


FIG. 4B

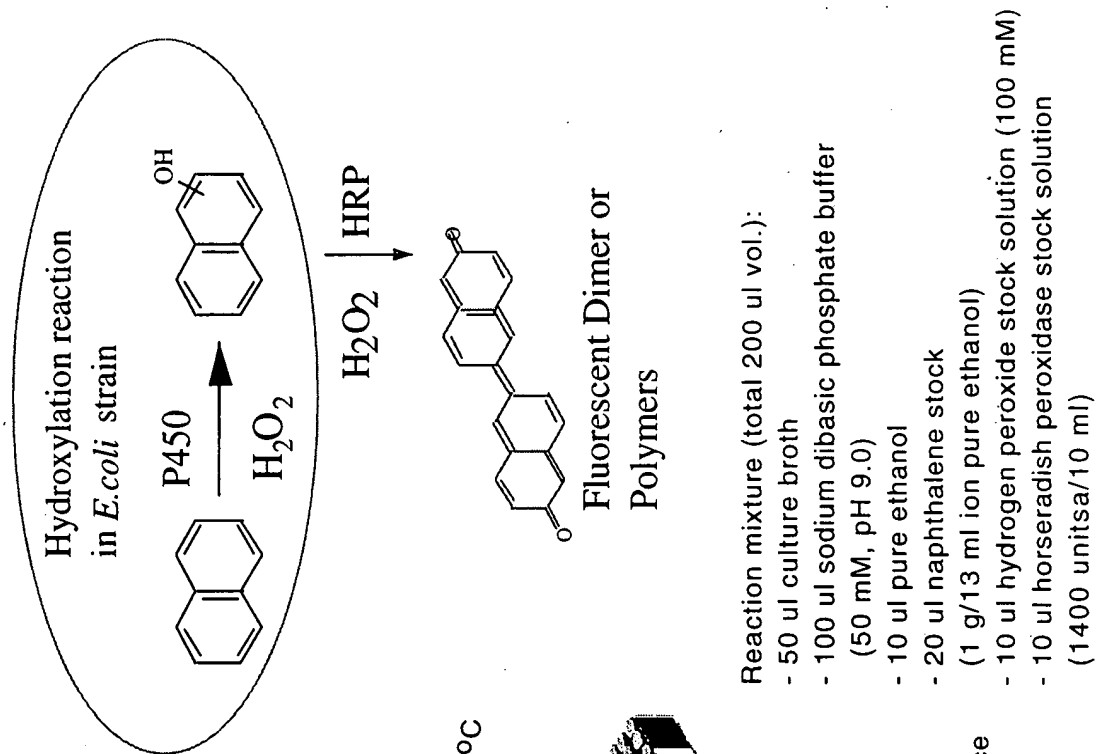


FIG. 5A

	1	2	3	4	5	6	7	8	9	10	11	12
A	2x			2x			2x			2x		
B	2x			2x	pCWori + P450cam		2x			2x		
C	2x			2x			2x			2x		
D	2x			2x			2x			2x		
E	2x			2x			2x			2x		
F	2x			2x	XL-10 <i>E.coli</i> strain		2x			2x		
G	2x			2x			2x			2x		
H	2x			2x			2x			2x		

TB +
0.5 mM delta ALA

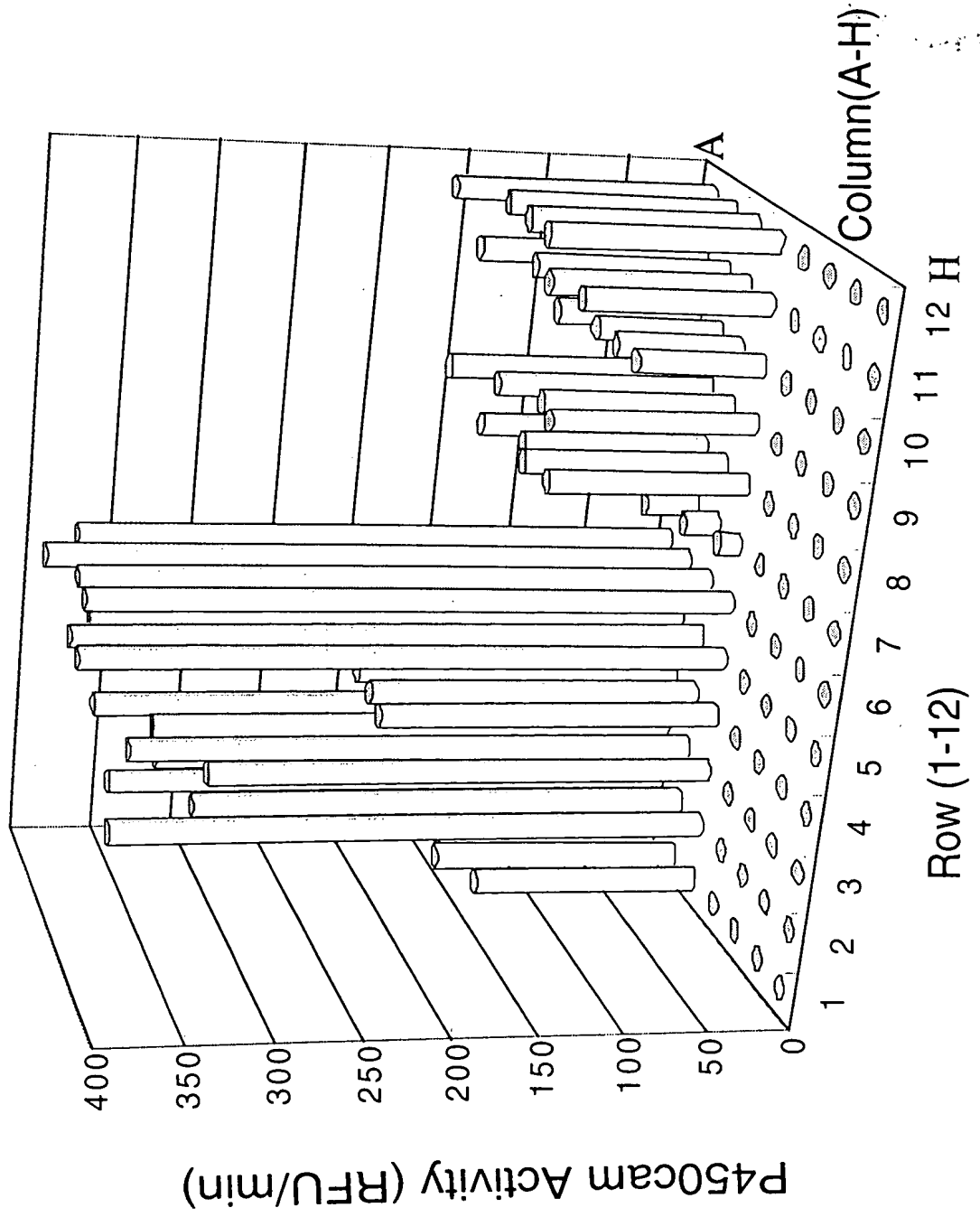
TB +
1.3 mM delta ALA

M9 (glucose) +
0.5 mM delta ALA

M9 (glycerol) +
0.5 mM delta ALA

* 2x : 200 ul cultivation volume, others : 100 ul cultivation volume

FIG. 5B



E.coli transformed with
pCWori (+)_P45Ocam &
pETpeIBHRPIA6Kan

FIG. 6

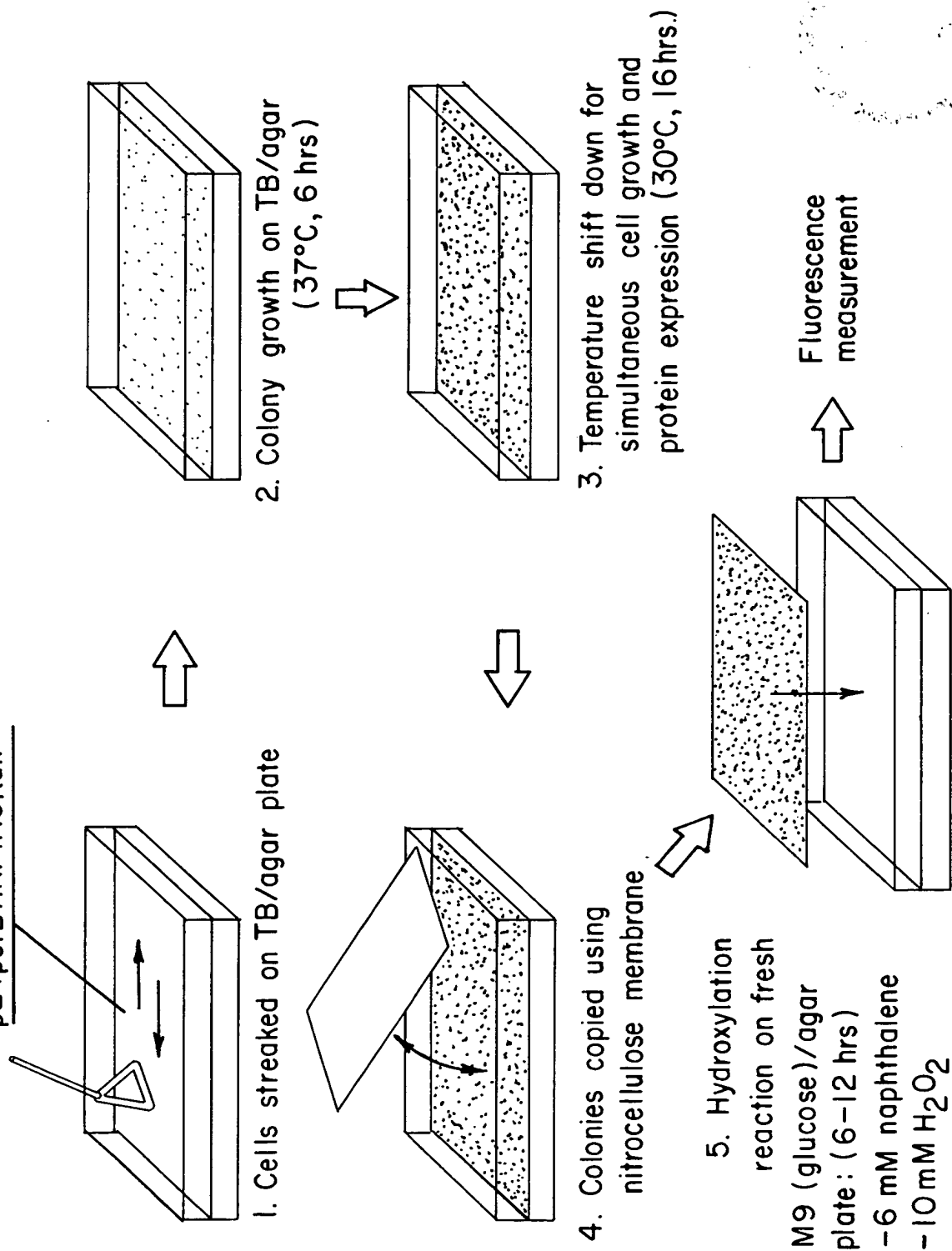


FIG. 7

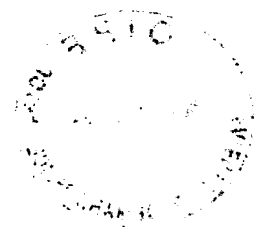
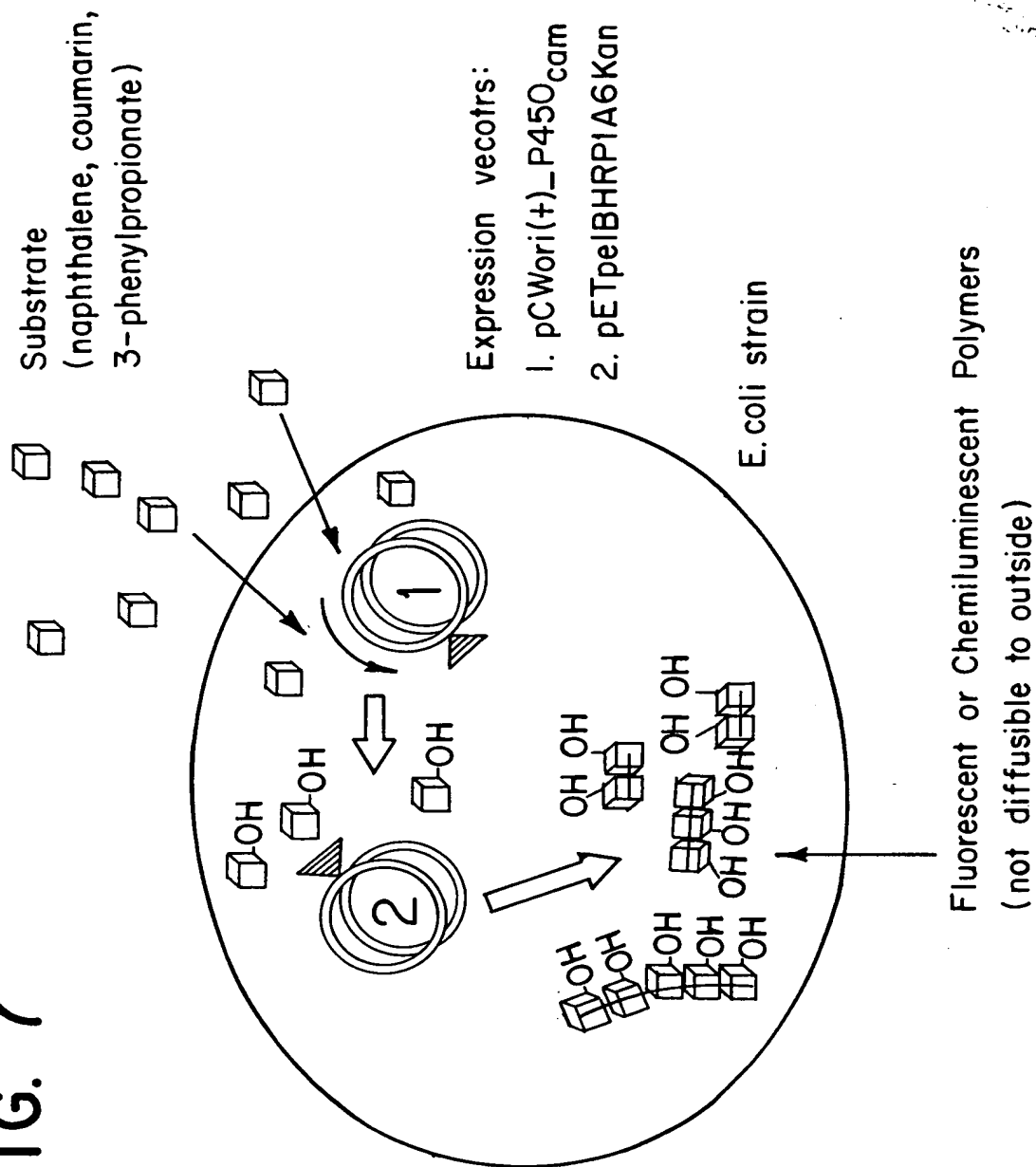


FIG. 8

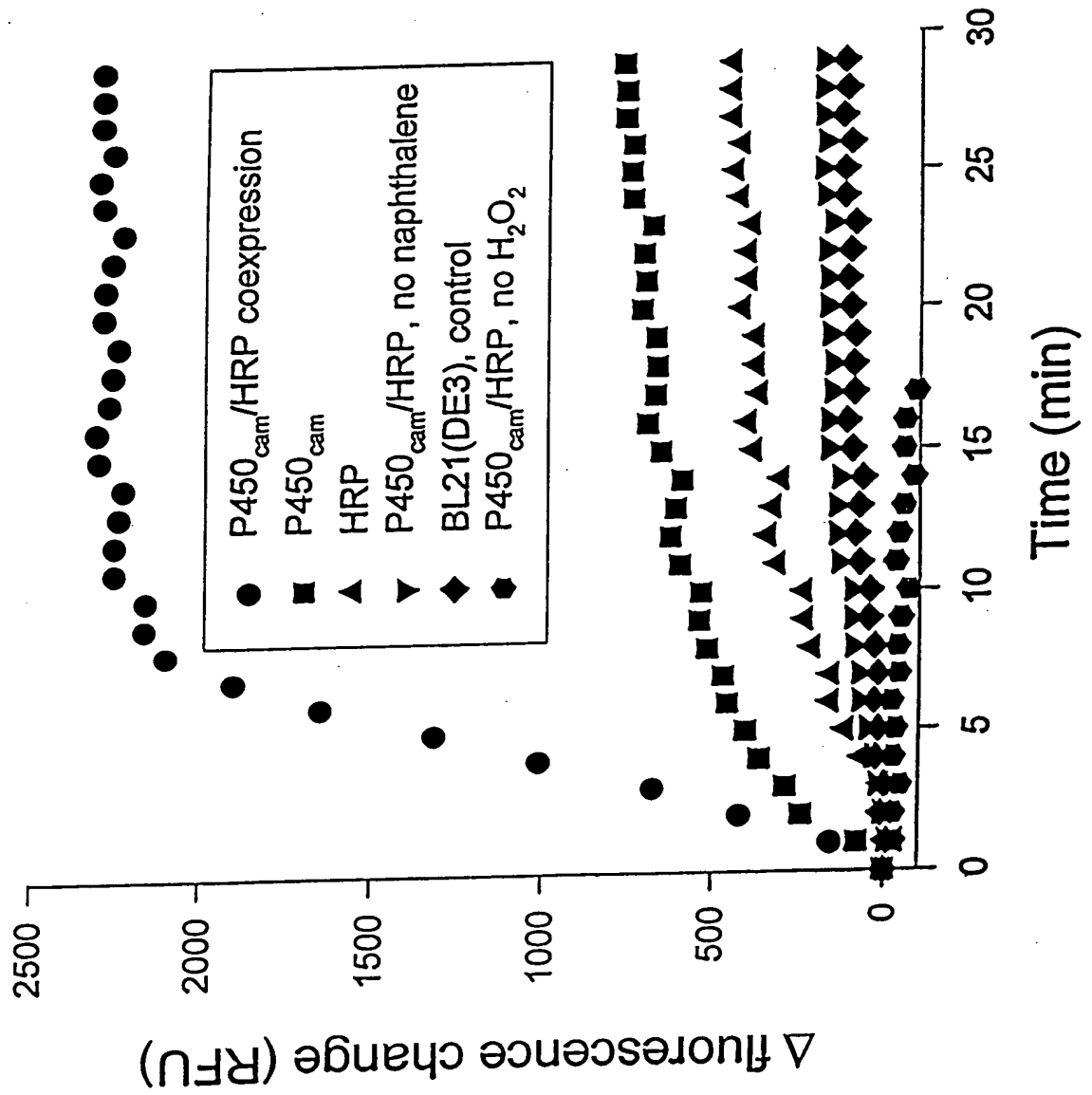
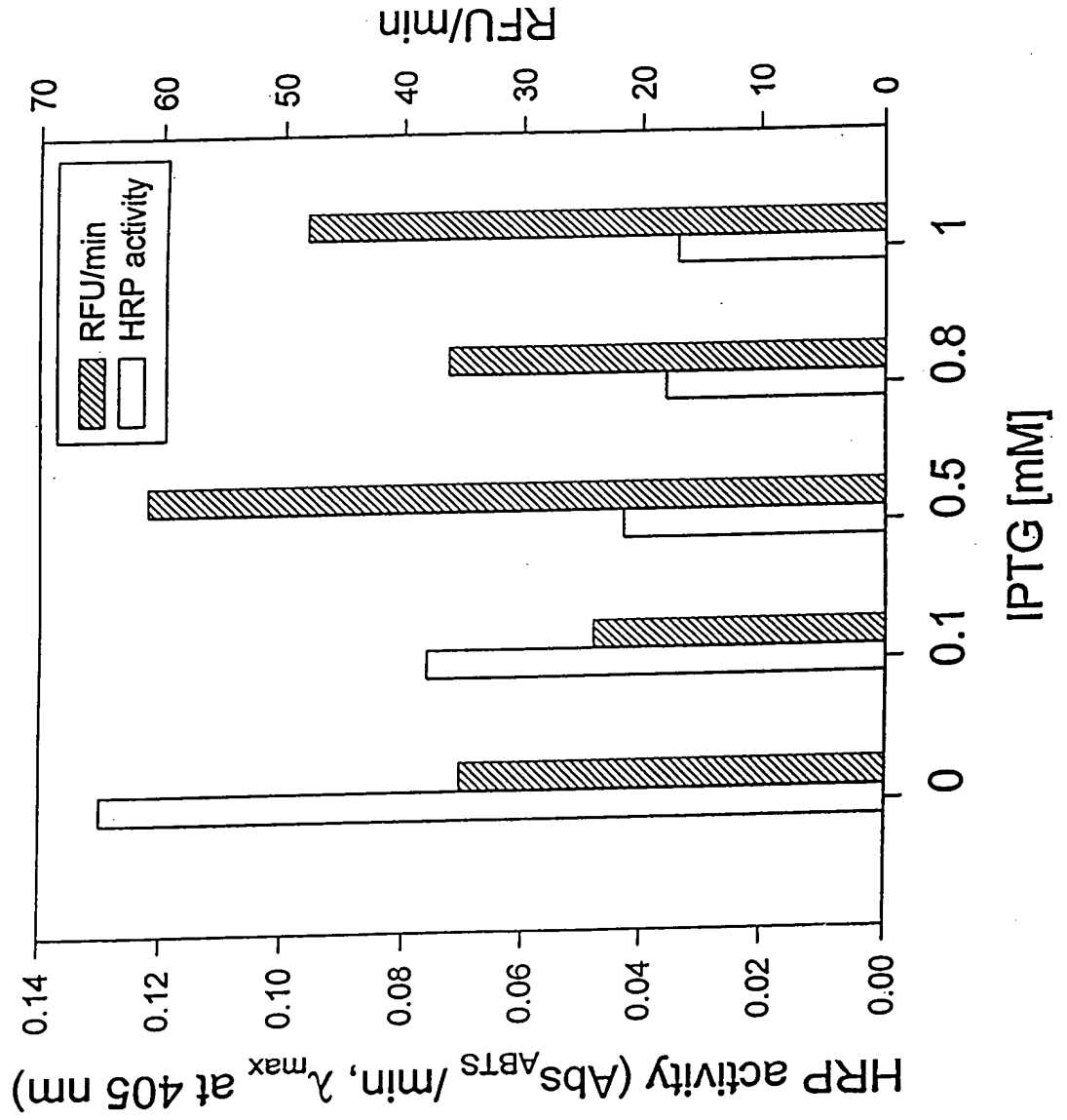


FIG. 9



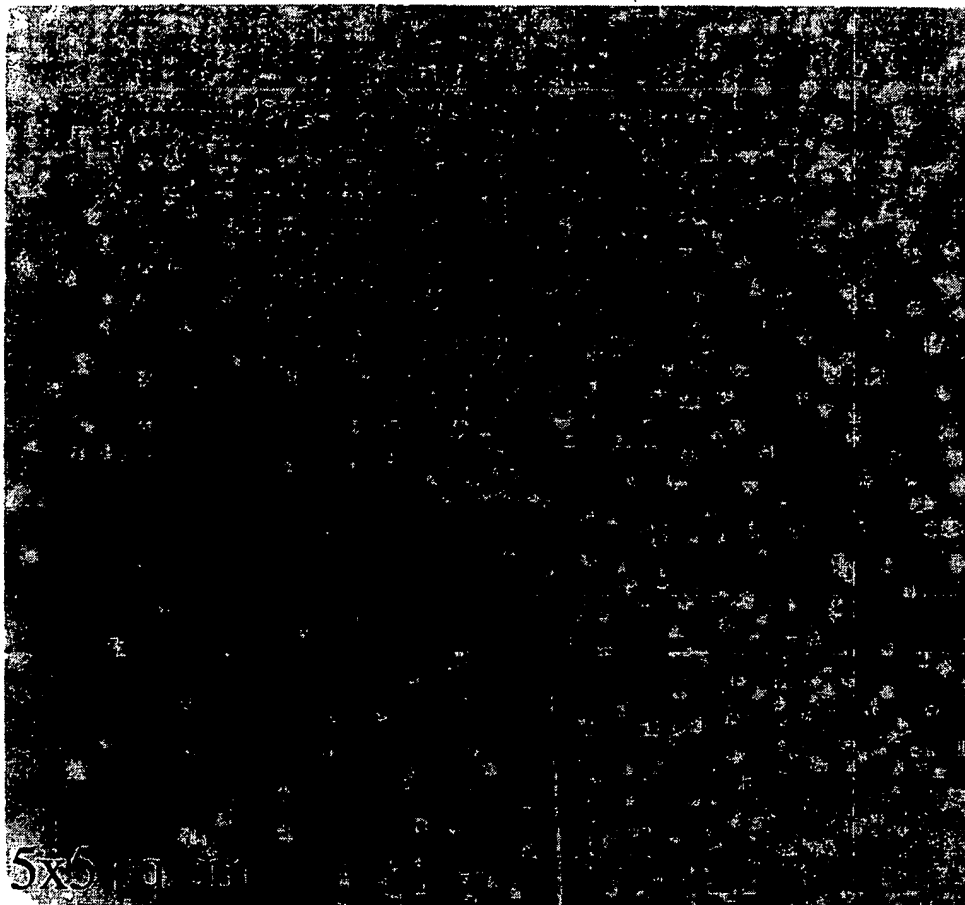


FIG. 12A

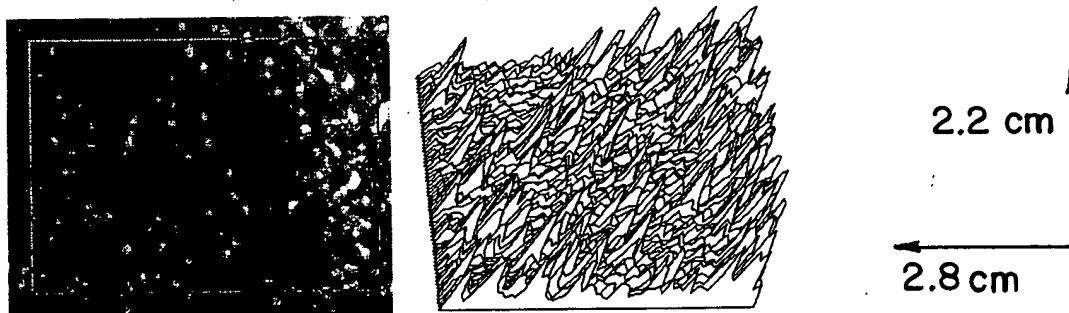


FIG. 12B

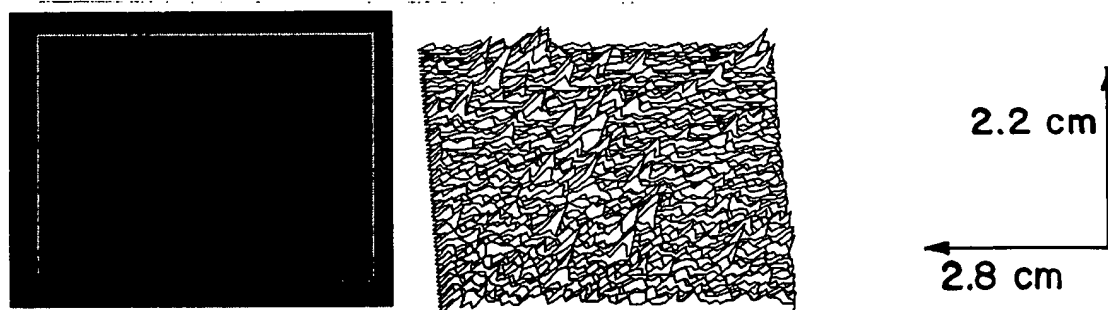




FIG. IIA

FIG. IIB

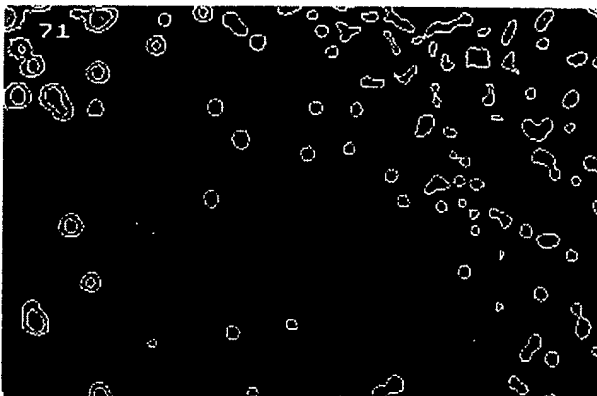
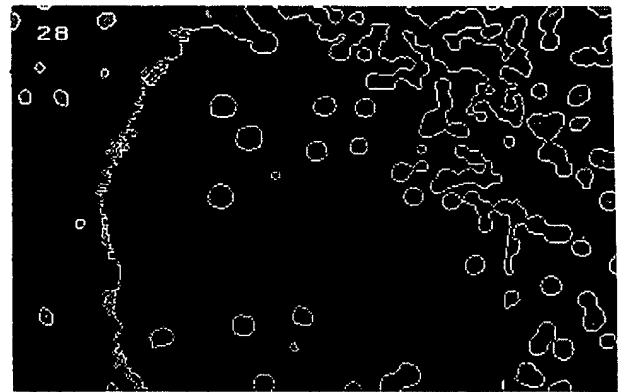


FIG. IIC

FIG. IID

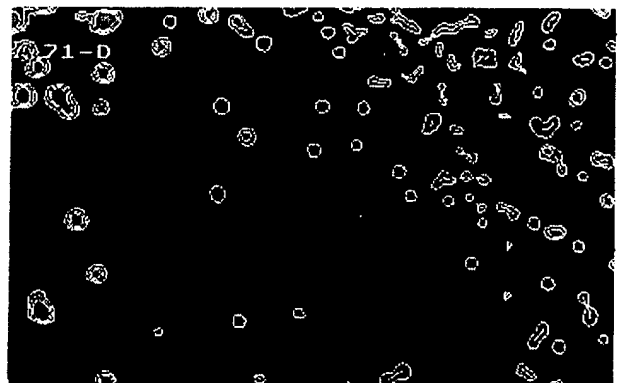


FIG. 12C

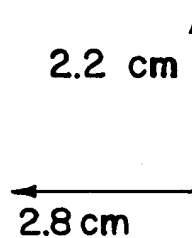
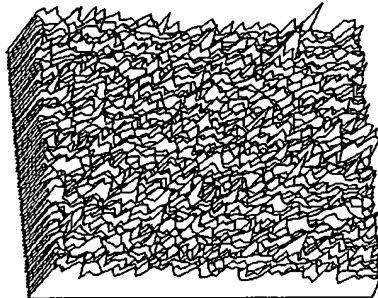
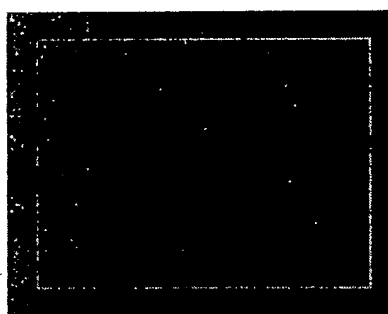


FIG. 12D

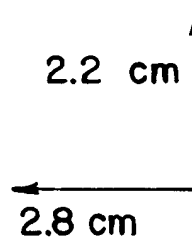
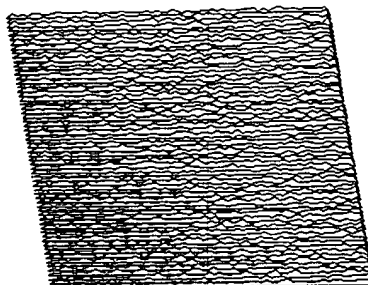
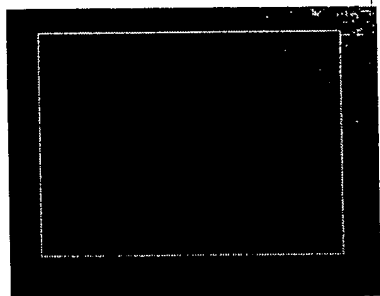


FIG. 12E

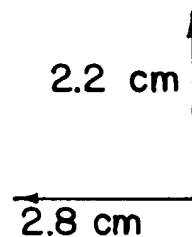
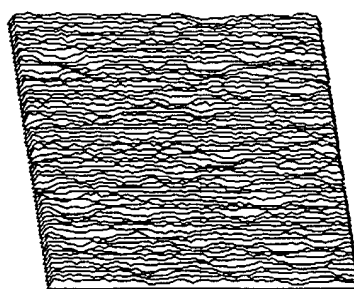
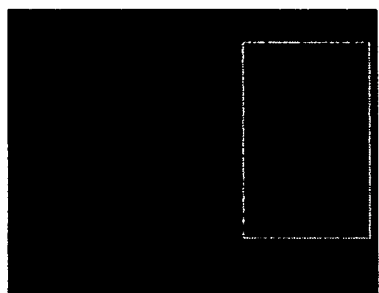


FIG. 12F

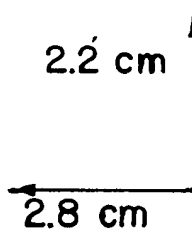
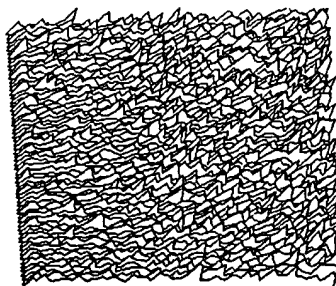
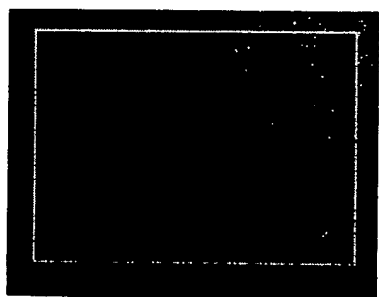
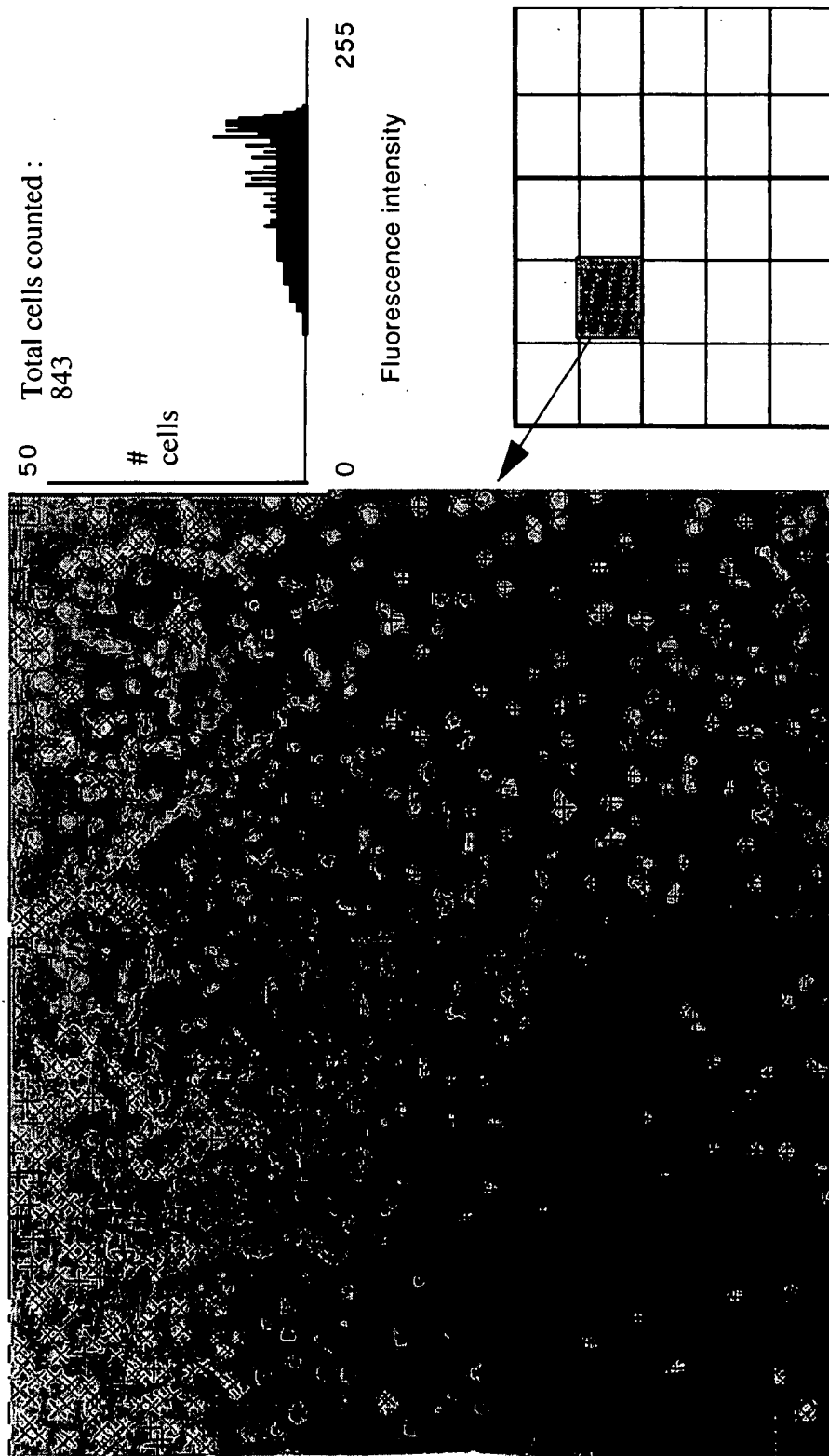


FIG. 13



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FIG. 14A

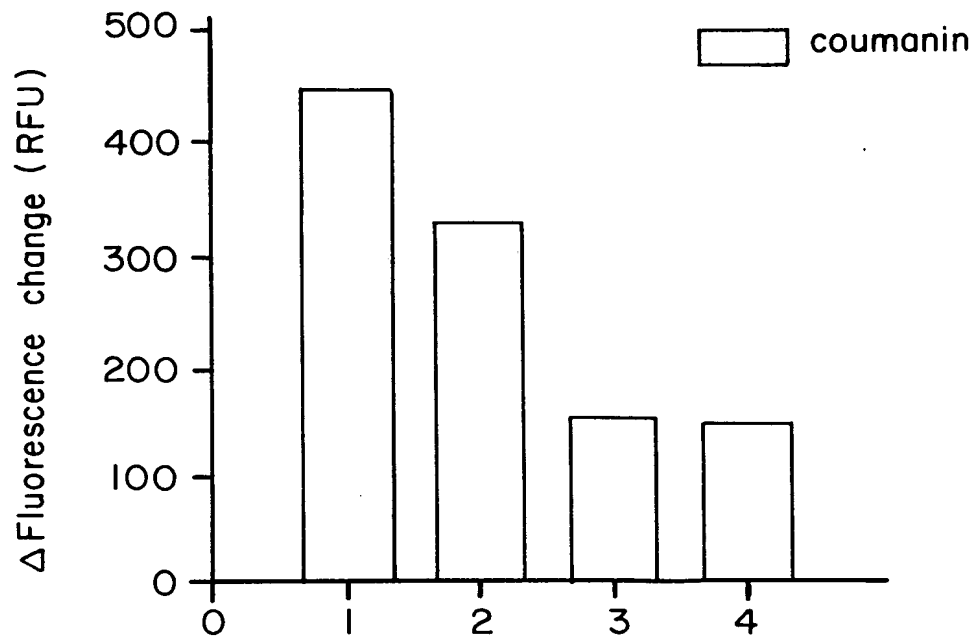


FIG. 14B

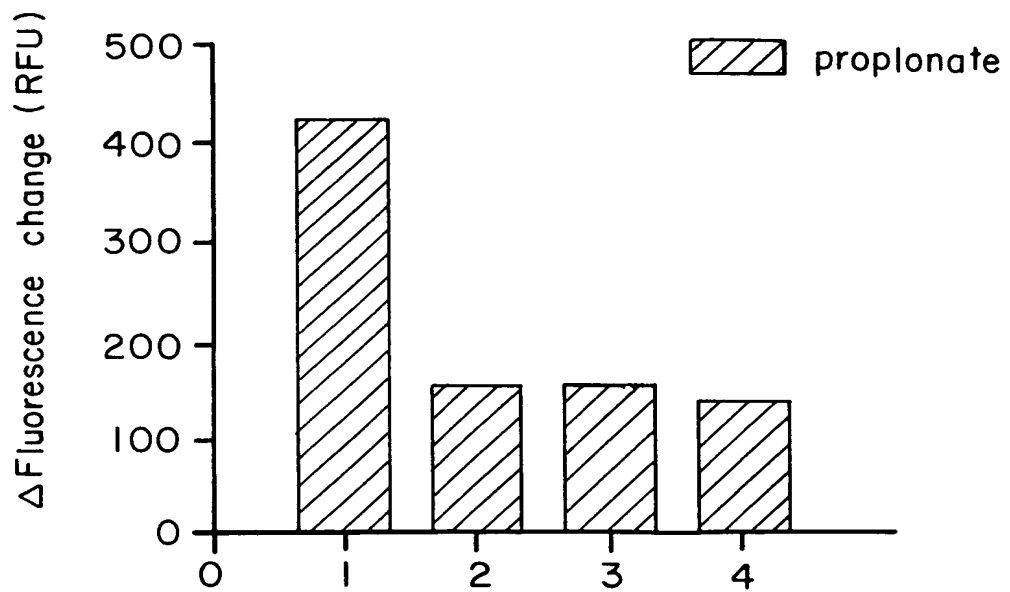
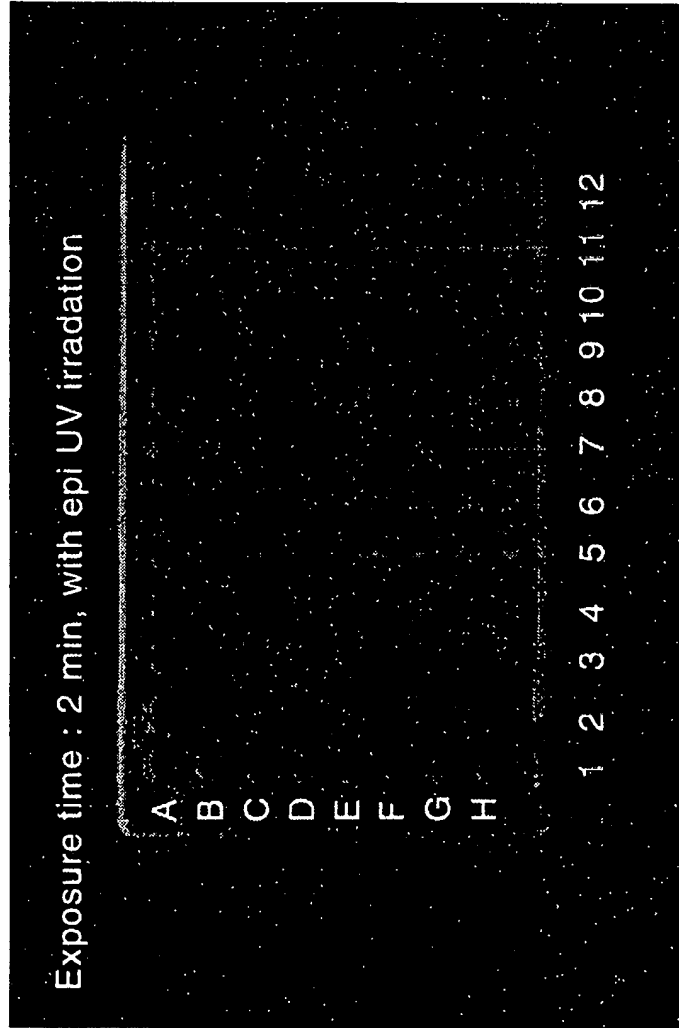


FIG. 15A



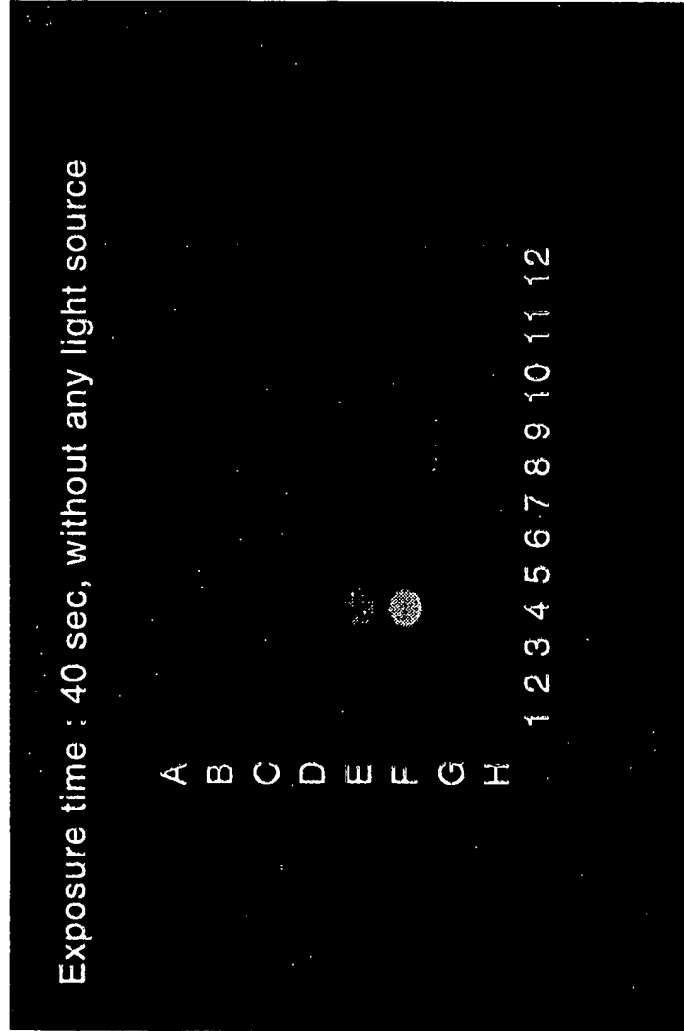
Row:

E: 60uM luminol+0.5 mM PPP
 F: 120 uM luminol+0.5 mM PPP
 G: 60 uM luminol
 H: 120 uM luminol

Column:

4: P450cam/HRP1A6 in
 BL21 (DE3)
 5: P450cam in BL21 (DE3)
 6: HRP1A6 in BL21 (DE3)
 7: Host strain, BL21 (DE3)

FIG. 15B



Light Emission Values

E4: 51 ILDV

F4: 98 ILDV

G4: 0.2 ILDV

H4: 1 ILDV

Others: <0.1 ILDV

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FIG. 17

- BL21 (DE3), control
- p450 cam
- △ CCP
- P450cam/CCP, (-) naphthalene
- P450cam/CCP

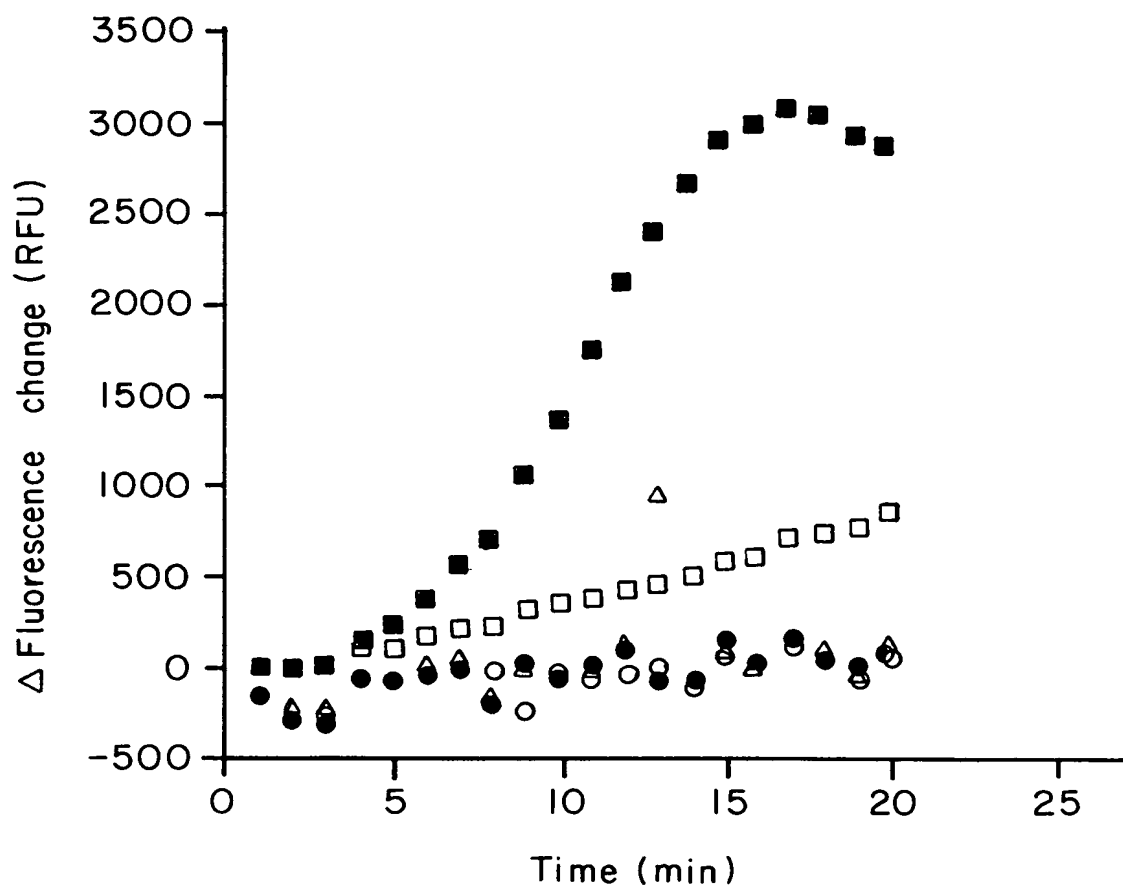


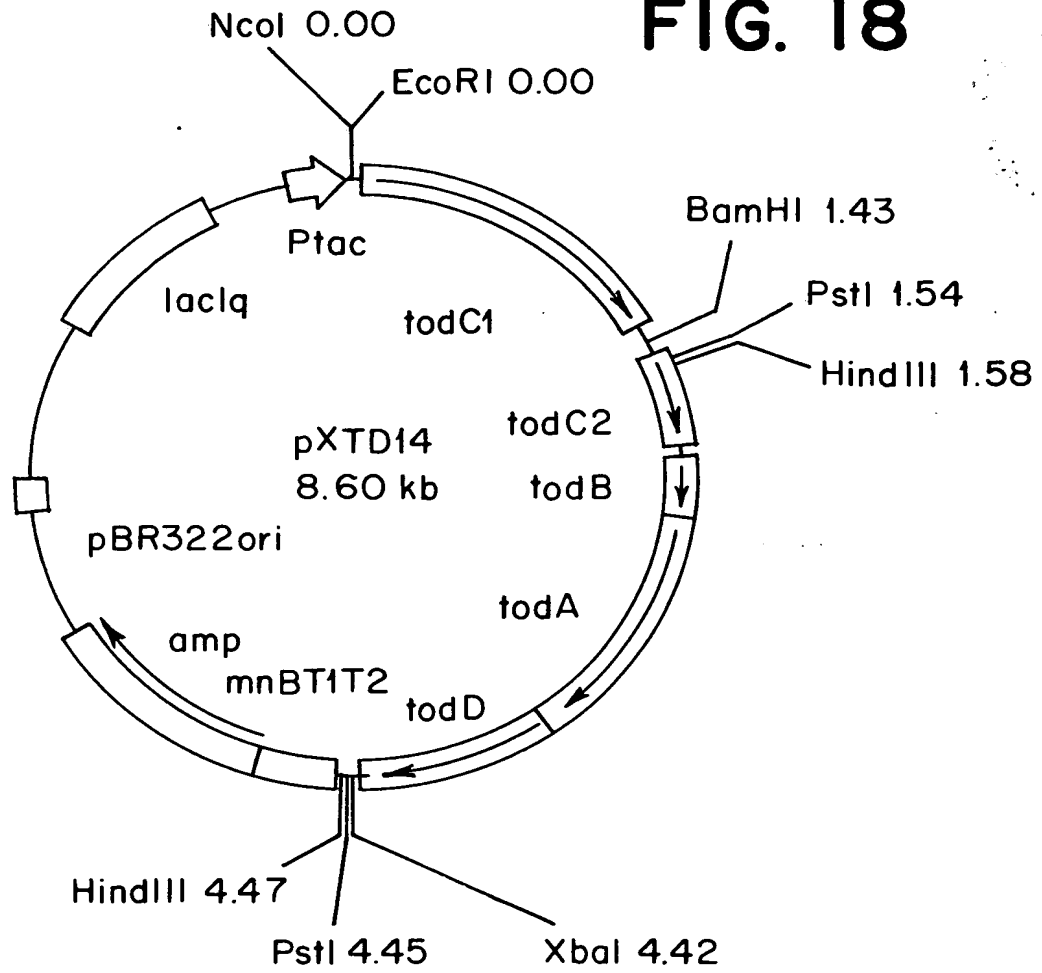
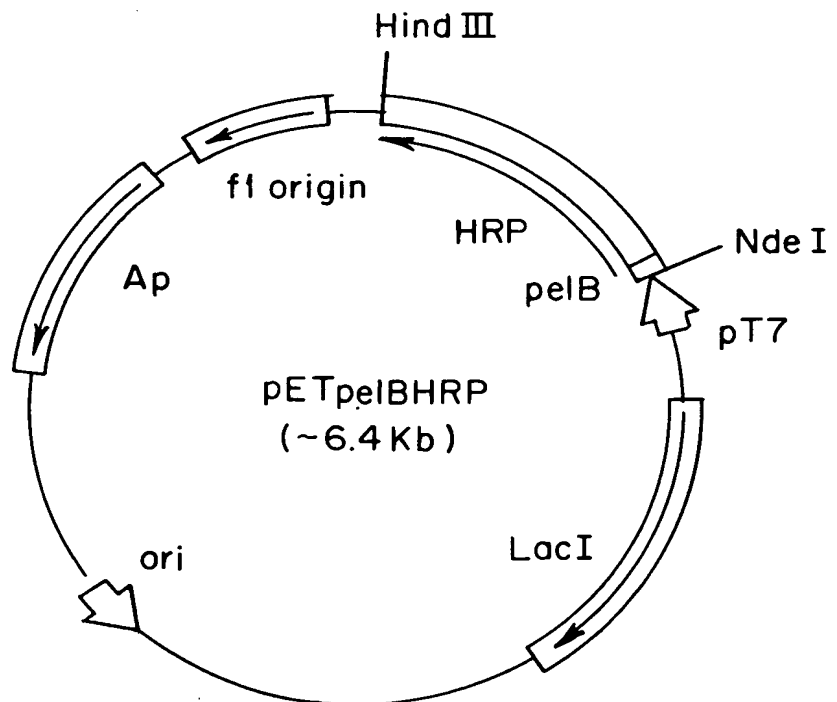
FIG. 18**FIG. 21**

FIG. 19A

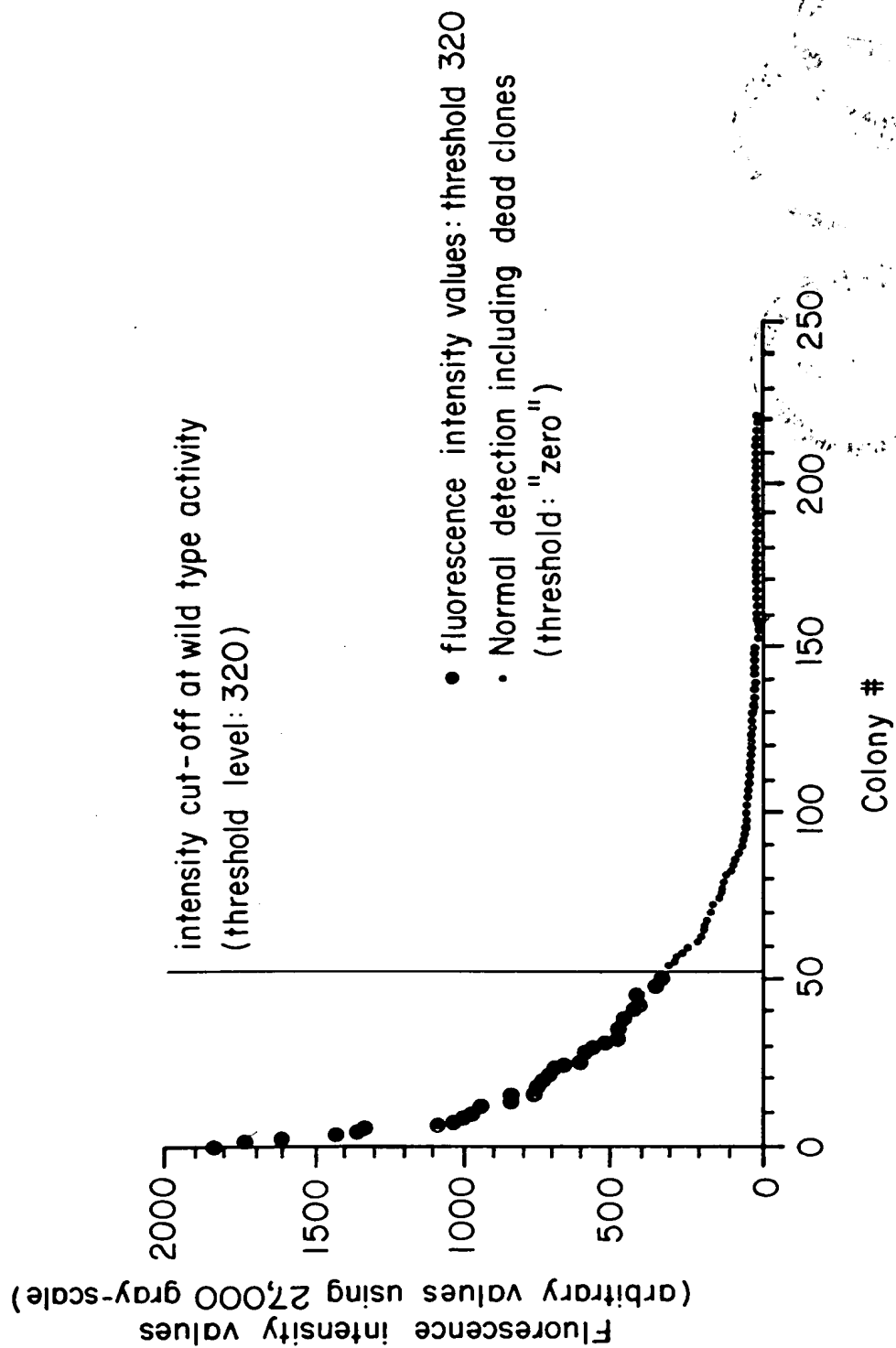
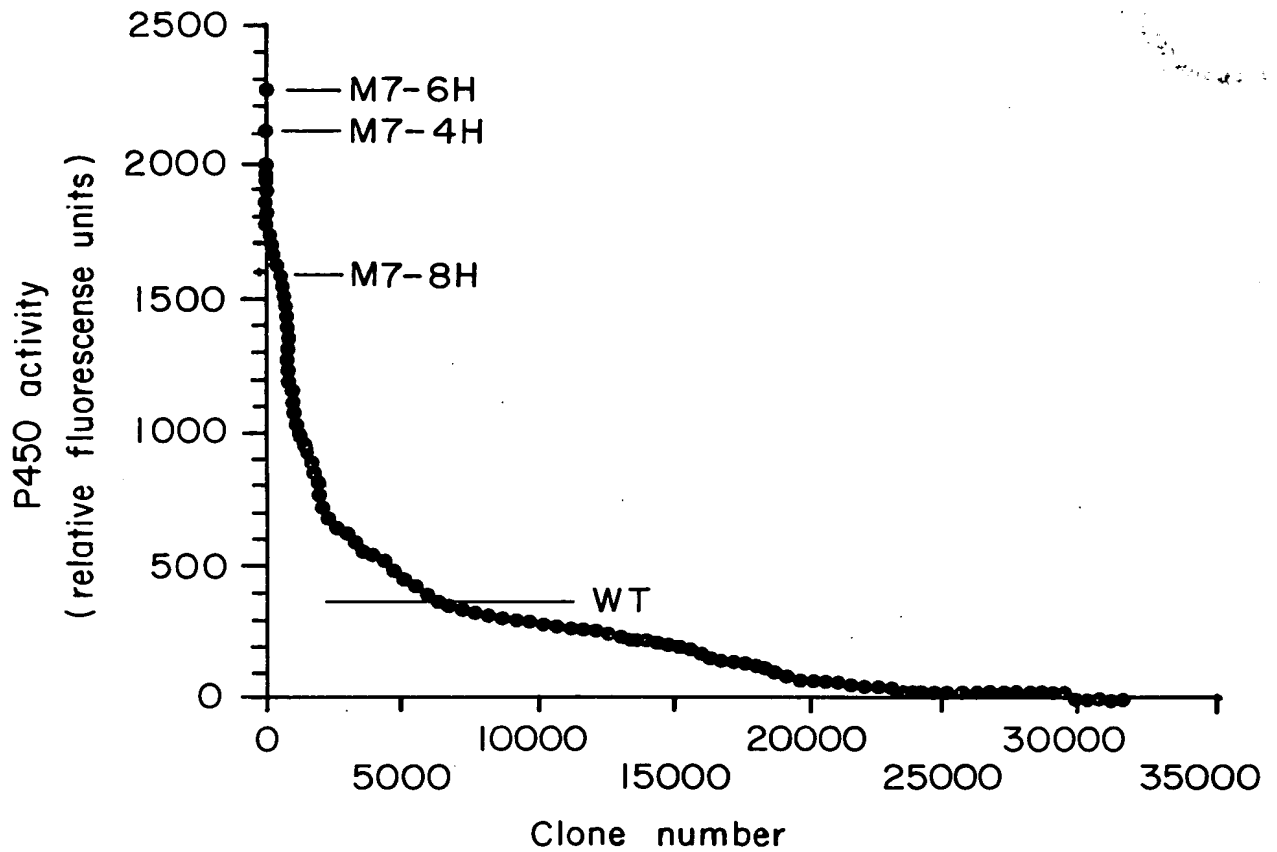
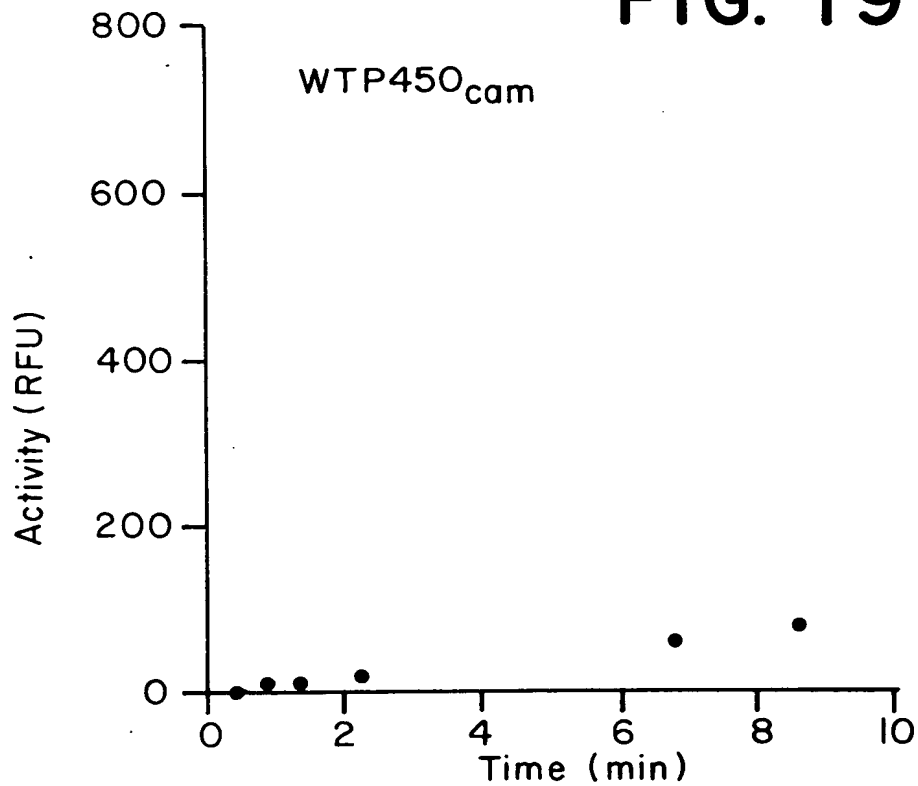


FIG. 19B**FIG. 19C**

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FIG. 19D

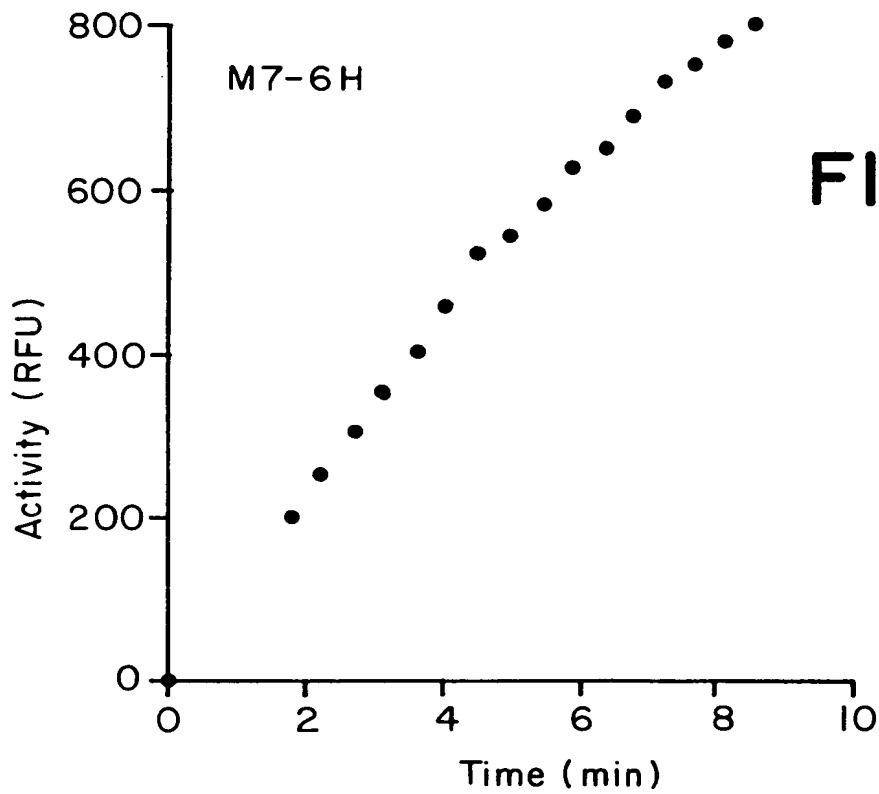
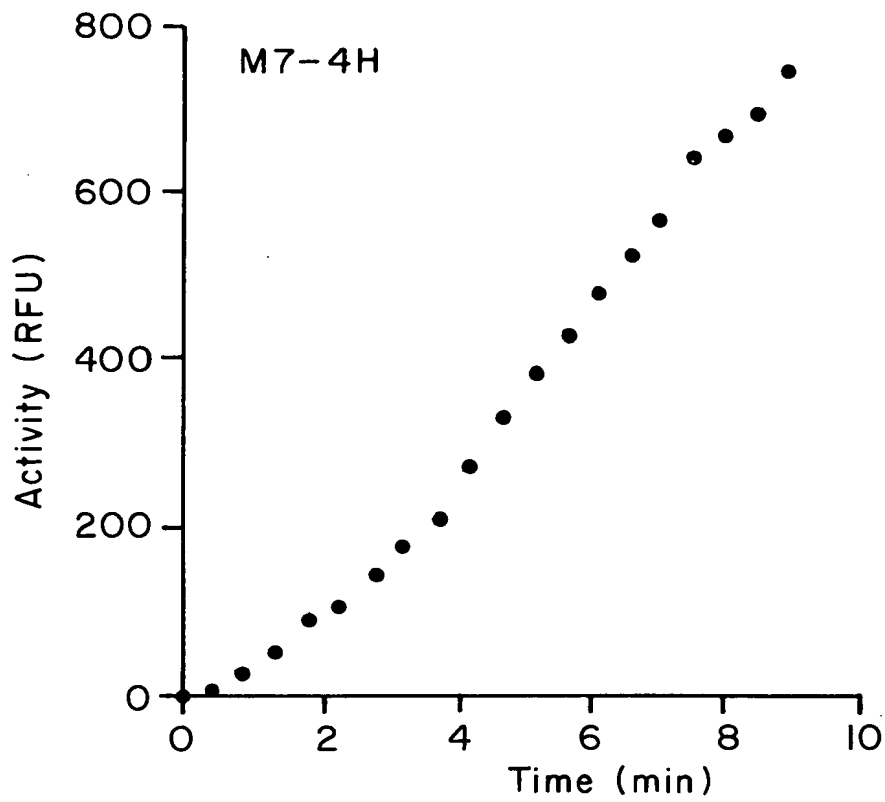


FIG. 19E

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FIG. 19 F

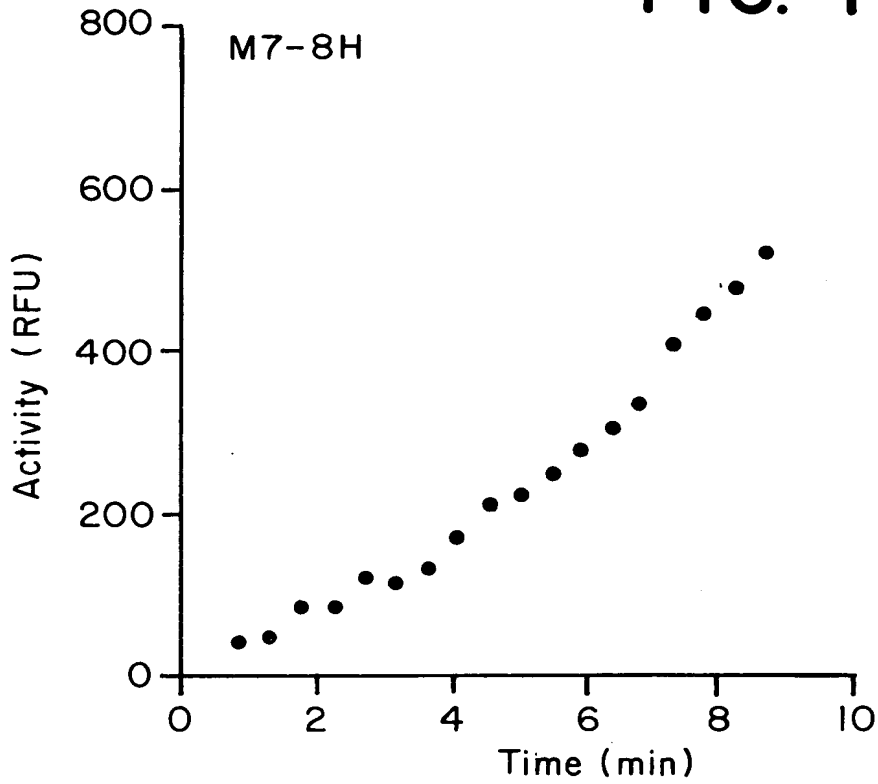


FIG. 20

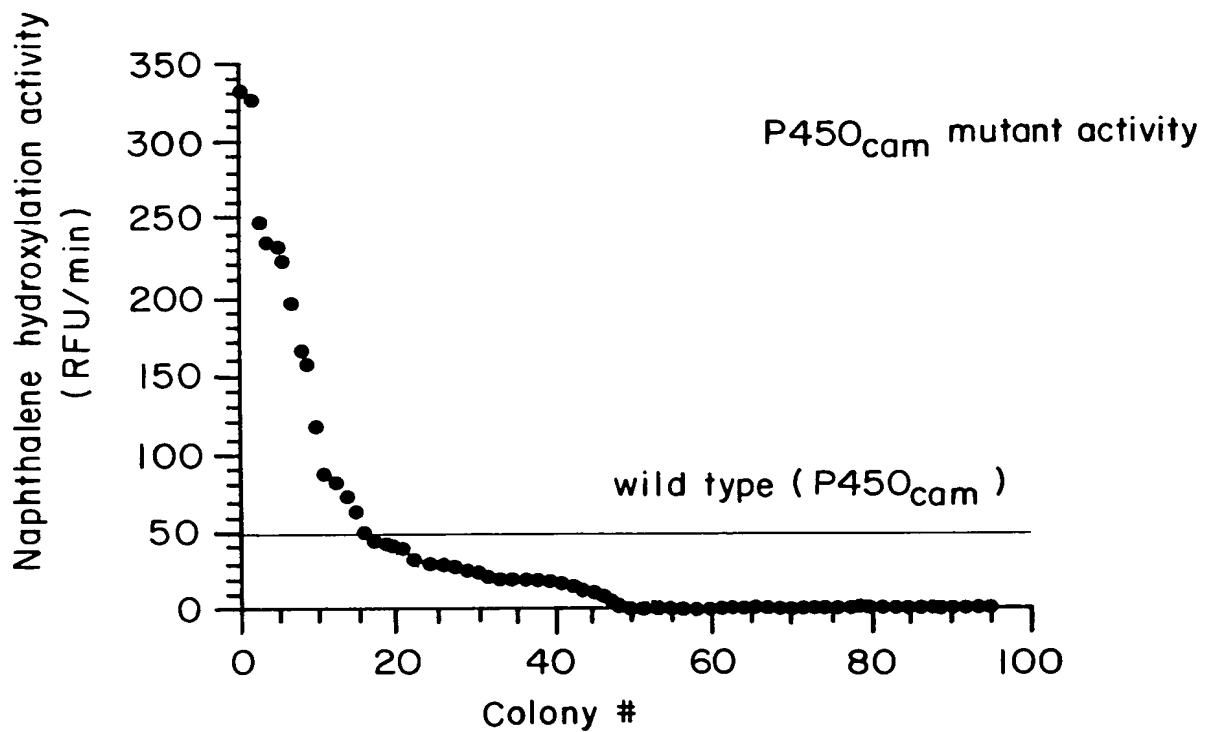


FIG. 22

ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC GCT GCC CAA CCA GCC ATG GCC
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala Ala Gln Pro Ala Met Ala

FIG. 23A

10 20 30 40 50 60
ATGCAGTTAACCCCTACATTCTACGACAATAGCTGTCCCAACGTTGCCAACATCGTTGGC

M Q L T P T F Y D N S C P N V S N I V R

70 80 90 100 110 120
GACACAATCGTCAACGAGCTCAGATCCGATCCCGAGGATCGCTGCTTCAATATACGTCCTG
D T I V N E L R S D P R I A A S I L R L

130 140 150 160 170 180
CACTTCCATGACTGCTTCGTGAATGGTTGGAGCGCTAGCATATTA CTGGACAACACCACC
H F H D C F V N G C D A S I L L D N T T

190 200 210 220 230 240
AGTTTCCGCACTGAAAAGGATGCATTCGGGAACGCTAACAGCGCCAGGGGCTTTCCAGTG
S F R T E K D A F G N A N S A R G F P V

A-----A

FIG. 23B

A-----A

250 260 270 280 290 300
ATCGATCGCATGAAGGCTGCCGTTGAGTCAGCATGCCACGAACAGTCAGTTGTGCAGAC
I D R M K A A V E S A C P R T V S C A D

310 320 330 340 350 360
CTGCTGACTATAGCTGCGCAACAGAGCGTGACTCTTGCAGGGCGGACCGTCTCTGGAGAGTG
L L T I A A Q Q S V T L A G G P S W R V

370 380 390 400 410 420
CCGCTCGGTGACGTGACTCCCTACAGGCGATTCCTAGATCTGGCCAAAGCCAACTTGCCT
P L G R R D S L Q A F L D L A N A N L P

430 440 450 460 470 480
GCTCCATTCTTCAACCCTGCCCCAGCTGAAGGATAGCTTTAGAAACGTGGGTCTGAATCGC
A P F F T L P Q L K D S F R N V G L N R

490 500 510 520 530 540
TCGAGTGACCTTGTGGCTCTGTCCGGAGGACACACATTTGGAAAGAACCCAGTGTAGGTTTC
S S D L V A L S G G H T F G K N Q C R F

B-----B

FIG. 23C

B-----B

550 560 570 580 590 600
ATCATGGATAGGCTCTACAATTTCAGCAACACTGGGTACCTGACCCACGCTGAACACT
I M D R L Y N F S N T G L P D P T L N T

610 620 630 640 650 660
ACGTATCTCCAGACACTGAGAGGCTTGTGCCACTGAATGGCAACCTCAGTGCACTAGTG
T Y L Q T L R G L C P L N G N L S A L V

670 680 690 700 710 720
GACTTTGATCTGCGGACCCCAACCATCTTCGATAACAAGTACTATGTGAATCTAGAGGAG
D F D L R T P T I F D N K Y Y V N L E E

730 740 750 760 770 780
CAGAAAGGCCTGATACAGAGTGATCAAGAAGTGTAGCAGTCCAGACGCCACTGACACC
Q K G L I Q S D Q E L F S S P D A T D T

790 800 810 820 830 840
ATCCCACTGGTGAGAAAGTTTGTAACTCTACTCAAAACCTTCTTTAACGCCCTTCGTGGAA
I P L V R S F A N S T Q T F F N A F V E

850 860 870 880 890 900
GCCATGGACCGTATGGGTAACATTACCCCTCTGACGGGTACCCAGGCCAGATTCTGTCTG
A M D R M G N I T P L T G T Q G Q I R L

910 920 930
AACTGCAGAGTGGTCAACAGCAACTCT
N C R V V N S N S

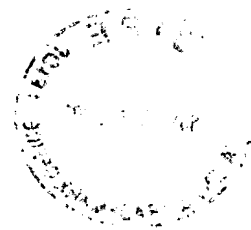
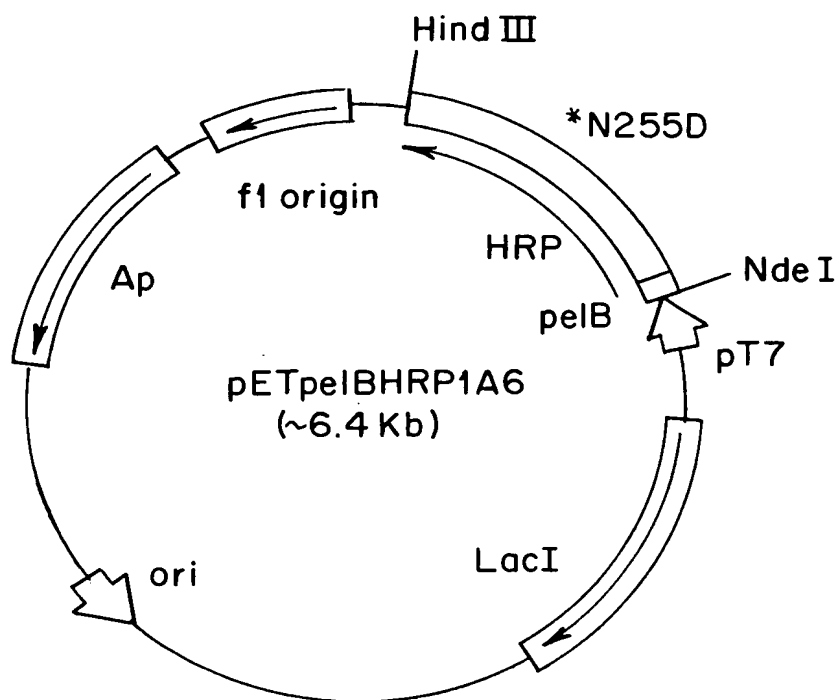


FIG. 24**FIG. 25**